

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:09:17 ; Search time 299.73 Seconds
(without alignments)
244.403 Million cell updates/sec

Title: US-09-331-631A-5
Perfect score: 3326
Sequence: 1 OCMOLETSGQMRVCVSCQDK.....SPRSRKQOQPLVSLIDFVGF 625

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP:REMBL_15:*
2: SP:archaea:*
3: SP_bacteria:*
4: SP_fungi:*
5: SP_human:*
6: SP_mammal:*
7: SP_minc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unklassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|--------------------|
| 1 | 3326 | 100.0 | 625 | 10 | Q9SP13 macadamia i |
| 2 | 3327 | 97.0 | 666 | 10 | Q9SP15 macadamia i |
| 3 | 3215 | 96.7 | 666 | 10 | Q9SP14 macadamia i |
| 4 | 1310.5 | 39.4 | 593 | 10 | Q9SEW4 juglans reg |
| 5 | 1163 | 35.0 | 810 | 10 | Q9ZWI3 cucurbita m |
| 6 | 1015 | 30.5 | 525 | 10 | Q43358 theobroma c |
| 7 | 888 | 26.7 | 582 | 10 | Q03865 zea mays (m |
| 8 | 864.5 | 26.0 | 637 | 10 | Q03678 hordeum vul |
| 9 | 844.5 | 25.4 | 613 | 10 | Q9M3X6 pisum sativ |
| 10 | 827 | 24.9 | 544 | 10 | Q22120 glycine max |
| 11 | 811 | 24.4 | 545 | 10 | Q41674 vicia narbo |
| 12 | 777.5 | 23.4 | 489 | 10 | Q9SP11 glycine max |
| 13 | 775.5 | 23.3 | 483 | 10 | Q49927 pisum sativ |
| 14 | 758 | 22.8 | 417 | 10 | Q22121 glycine max |
| 15 | 757.5 | 22.8 | 438 | 10 | Q43626 pisum sativ |
| 16 | 749.5 | 22.5 | 463 | 10 | Q41677 vicia narbo |
| 17 | 747 | 22.5 | 486 | 10 | Q91UJ7 arabidopsis |
| 18 | 740 | 22.2 | 448 | 10 | Q40873 picea glauc |
| 19 | 729 | 21.9 | 450 | 10 | Q40844 picea glauc |

| | | | | | |
|----|-------|------|-----|----|---------------------|
| 20 | 709.5 | 21.3 | 518 | 10 | Q9M3X8 lens culina |
| 21 | 649 | 19.5 | 461 | 10 | Q9ZRG9 oryza sativ |
| 22 | 560 | 16.8 | 430 | 10 | Q41115 phaseolus v |
| 23 | 558.5 | 16.8 | 414 | 10 | Q41727 zania furfu |
| 24 | 556 | 16.7 | 430 | 10 | Q43633 phaseolus v |
| 25 | 549 | 16.5 | 421 | 10 | Q43632 phaseolus v |
| 26 | 541.5 | 16.3 | 232 | 10 | Q9SQ49 rullingia ma |
| 27 | 532.5 | 16.0 | 540 | 10 | Q03866 zea mays (m |
| 28 | 527.5 | 15.9 | 423 | 10 | Q43617 phaseolus l |
| 29 | 527 | 15.8 | 239 | 10 | Q9SQ50 abroma angu |
| 30 | 522 | 15.7 | 239 | 10 | Q9SQ42 theobroma b |
| 31 | 521.5 | 15.7 | 236 | 10 | Q9SQ41 theobroma b |
| 32 | 521.5 | 15.7 | 428 | 10 | Q40913 phaseolus l |
| 33 | 521 | 15.7 | 238 | 10 | Q9SQ32 theobroma s |
| 34 | 520.5 | 15.6 | 236 | 10 | Q9SQ47 theobroma s |
| 35 | 520 | 15.6 | 239 | 10 | Q9SQ44 theobroma v |
| 36 | 518.5 | 15.6 | 236 | 10 | Q9SQ40 theobroma c |
| 37 | 517.5 | 15.6 | 236 | 10 | Q9SQ36 theobroma g |
| 38 | 517.5 | 15.6 | 236 | 10 | Q9SQ34 theobroma m |
| 39 | 516.5 | 15.5 | 239 | 10 | Q9SQ37 theobroma g |
| 40 | 516 | 15.5 | 239 | 10 | Q9SQ35 theobroma c |
| 41 | 516 | 15.5 | 239 | 10 | Q9SQ79 theobroma c |
| 42 | 515.5 | 15.5 | 236 | 10 | Q9SQ48 theobroma m |
| 43 | 515 | 15.5 | 239 | 10 | Q9SQ43 theobroma b |
| 44 | 510.5 | 15.3 | 236 | 10 | Q9SQ33 theobroma m |
| 45 | 508 | 15.3 | 235 | 10 | Q9SQ38 theobroma g |

ALIGNMENTS

RESULT 1
ID Q9SP13 PRELIMINARY: PRT: 625 AA.
AC Q9SP13;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE VICILIN PRECURSOR (FRAGMENT).
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
OC NCBI_TaxID=60698;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NOT KNOWN.
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
RT globulin protein in Macadamia integrifolia.";
RL Plant J. 0:0-0(1999).
DR EMBL: AF161885; MADS4246.1; -.
DR HSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -.
DR PFM: PF00546; Seedstore_7s; 1.
FT NON_TER
SQ SEQUENCE 625 AA: 73586 MW: 415808489D370296 CRC64:

Query Match 100.0%; Score 3326; DB 10; Length 625;
Best Local Similarity 100.0%; Pred. No. 7.7e-236;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 OCMOLETSGQMRVCVSCQDKREEDIDWSKYNOEDPOTECQCCQRCRQOQESDPRQOY 60
DB 1 OCMOLETSGQMRVCVSCQDKREEDIDWSKYNOEDPOTECQCCQRCRQOQESDPRQOY 60
QY 61 CORRKEICEEEFEYNRQDPOQYEQCCRCORRETEPRHMOICQORCERRYERKRRQ 120
DB 61 CORRKEICEEEFEYNRQDPOQYEQCCRCORRETEPRHMOICQORCERRYERKRRQ 120
QY 121 ORYREQOQREDEKYEERKKEGDNKRDPQOQREYEDCRHRECEQDEPRLOYOCORCQOQOR 180
DB 121 ORYREQOQREDEKYEERKKEGDNKRDPQOQREYEDCRHRECEQDEPRLOYOCORCQOQOR 180

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Db 121 QKRYEQREDEEKYEERKKEGDNKRDPOQREYEDCRRHCEQOEPRLOYOCORRCEQOR 180
QY 181 QHGRGDDLNNPORGSGRGYEEGEKOSDNPYYFDEKSLSTRFTEBGHISVLENFYGRSK 240
Db 181 QHGRGDDLNNPORGSGRGYEEGEKOSDNPYYFDEKSLSTRFTEBGHISVLENFYGRSK 240
QY 241 LRLAKNRYLVLEANNPNAFVLPHTLDADAILLVIGRGALKMIRHNDRESYNLECGDYI 300
Db 241 LRLAKNRYLVLEANNPNAFVLPHTLDADAILLVIGRGALKMIRHNDRESYNLECGDYI 300
QY 301 RIPAGTFFYLINRDNNEERLHIAKFLQITSTPGQYKEFFPAGGONPEPYLSTFSKELLEA 360
Db 301 RIPAGTFFYLINRDNNEERLHIAKFLQITSTPGQYKEFFPAGGONPEPYLSTFSKELLEA 360
QY 361 LNTQTERLGVGLGOOREGYIIRASQEQIRELTREDSESRWHIRRGESSRGYPYLPFKR 420
Db 361 LNTQTERLGVGLGOOREGYIIRASQEQIRELTREDSESRWHIRRGESSRGYPYLPFKR 420
QY 421 PLYSNKYGAYEYKPEPDYRQLODMDSVFITANTOGSMGPFENRSTKVVVVASGEADV 480
Db 421 PLYSNKYGAYEYKPEPDYRQLODMDSVFITANTOGSMGPFENRSTKVVVVASGEADV 480
QY 481 EMACPHLSGRHGGRGCGKRHEEEYHYEQVBARLSKREAIIVLAGHPVYVSSGNENLL 540
Db 481 EMACPHLSGRHGGRGCGKRHEEEYHYEQVBARLSKREAIIVLAGHPVYVSSGNENLL 540
QY 541 LFAFGINAONNHNENFLAGERNVLOOIEPOMELAFASRKEVEELFNSODESIFPPGPR 600
Db 541 LFAFGINAONNHNENFLAGERNVLOOIEPOMELAFASRKEVEELFNSODESIFPPGPR 600
QY 601 QHQOQSPRSTKQOQPLVSTILDFVGF 625
Db 601 QHQOQSPRSTKQOQPLVSTILDFVGF 625

RESULT 2
Q9SP15 PRELIMINARY: PRT: 666 AA.
AC Q9SP15:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR.
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
OX NCBI_TaxID=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NUT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
RT globulin protein in Macadamia integrifolia kernels.";
RL Plant J. 0:0-0(1999)
DR EMBL: AF161883; AAD54244.1; -
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -
DR PFAM: PF00546; Seedstore_7s; 1.
SQ SEQUENCE 666 AA: 78217 MW: C752B884B2DP0224 CRC64;
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Query Match 97.0%; Score 3227; DB 10; Length 666;
Best Local Similarity 96.6%; Pred. No. 1.5e-228;
Matches 604; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
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QY 1 OCMQLETSGOMRCVSCQCKRFEEDIDMSKYDQEDPOTECOCQORRQOESDPPQOY 60
Db 42 OCMQLETSGOMRCVSCQCKRFEEDIDMSKYDQEDPOTECOCQORRQOESDPPQOY 101
QY 61 CORRKEICEEEYNNRDPPOOYEQOCRCORRETEPHIMOICORRREYKERRK 120
Db 102 CORRKEICEEEYNNRDPPOOYEQOCRCORRETEPHIMOICORRREYKERRK 161
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QY 121 QKRYEQREDEEKYEERKKEGDNKRDPOQREYEDCRRHCEQOEPRLOYOCORRCEQOR 180
Db 162 QKRYEQREDEEKYEERKKEGDNKRDPOQREYEDCRRHCEQOEPRLOYOCORRCEQOR 221
QY 181 QHGRGDDLNNPORGSGRGYEEGEKOSDNPYYFDEKSLSTRFTEBGHISVLENFYGRSK 240
Db 222 QHGRGDDLNNPORGSGRGYEEGEKOSDNPYYFDEKSLSTRFTEBGHISVLENFYGRSK 281
QY 241 LRLAKNRYLVLEANNPNAFVLPHTLDADAILLVIGRGALKMIRHNDRESYNLECGDYI 300
Db 282 LRLAKNRYLVLEANNPNAFVLPHTLDADAILLVIGRGALKMIRHNDRESYNLECGDYI 341
QY 301 RIPAGTFFYLINRDNNEERLHIAKFLQITSTPGQYKEFFPAGGONPEPYLSTFSKELLEA 360
Db 342 RIPAGTFFYLINRDNNEERLHIAKFLQITSTPGQYKEFFPAGGONPEPYLSTFSKELLEA 401
QY 361 LNTQTERLGVGLGOOREGYIIRASQEQIRELTREDSESRWHIRRGESSRGYPYLPFKR 420
Db 402 LNTQTERLGVGLGOOREGYIIRASQEQIRELTREDSESRWHIRRGESSRGYPYLPFKR 461
QY 421 PLYSNKYGAYEYKPEPDYRQLODMDSVFITANTOGSMGPFENRSTKVVVVASGEADV 480
Db 462 PLYSNKYGAYEYKPEPDYRQLODMDSVFITANTOGSMGPFENRSTKVVVVASGEADV 521
QY 481 EMACPHLSGRHGGRGCGKRHEEEYHYEQVBARLSKREAIIVLAGHPVYVSSGNENLL 540
Db 522 EMACPHLSGRHGGRGCGKRHEEEYHYEQVBARLSKREAIIVLAGHPVYVSSGNENLL 581
QY 541 LFAFGINAONNHNENFLAGERNVLOOIEPOMELAFASRKEVEELFNSODESIFPPGPR 600
Db 582 LFAFGINAONNHNENFLAGERNVLOOIEPOMELAFASRKEVEELFNSODESIFPPGPR 641
QY 601 QHQOQSPRSTKQOQPLVSTILDFVGF 625
Db 642 QHQOQSPRSTKQOQPLVSTILDFVGF 666
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RESULT 3
Q9SP14 PRELIMINARY: PRT: 666 AA.
AC Q9SP14:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR.
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
OX NCBI_TaxID=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NUT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
RT globulin protein in Macadamia integrifolia.";
RL Plant J. 0:0-0(1999)
DR EMBL: AF161884; AAD54245.1; -
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -
DR PFAM: PF00546; Seedstore_7s; 1.
SQ SEQUENCE 666 AA: 78243 MW: DECA22F8710F8A7B CRC64;
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Query Match 96.7%; Score 3215; DB 10; Length 666;
Best Local Similarity 96.6%; Pred. No. 1.2e-227;
Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
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QY 1 OCMQLETSGOMRCVSCQCKRFEEDIDMSKYDQEDPOTECOCQORRQOESDPPQOY 60
Db 42 OCMQLETSGOMRCVSCQCKRFEEDIDMSKYDQEDPOTECOCQORRQOESDPPQOY 101
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QY 61 CORCKEICEEEENRORPDQOQYEDQCKRQRETEPRHMOICQCKERYKEKQK 120
D 102 CORCKEICEEEENRORPDQOQYEDQCKRQRETEPRHMOICQCKERYKEKQK 161
QY 121 OKREEOORREDEEYEEEMKEDGNKRDPOOREYEDCRHNCEOEPRLOYOCORCOBOOR 180
D 162 OKREEOORREDEEYEEEMKEDGNKRDPOOREYEDCRHNCEOEPRLOYOCORCOBOOR 221
QY 181 OHGKGDLMPORGSGSREYEEGEKOSDNPYFEDERLSTRFTEEGHISYLENFYRSK 240
D 222 OHGKGDLMPORGSGSREYEEGEKOSDNPYFEDERLSTRFTEEGHISYLENFYRSK 281
QY 241 LRLALKNRYLVLEPNAPNAEVLPTHLADALLVIGRGALKMHRDNRESYNLECGDVI 300
D 282 LRLALKNRYLVLEPNAPNAEVLPTHLADALLVIGRGALKMHRDNRESYNLECGDVI 341
QY 301 RIPAGTFYLLNRDNRRNLHIAKFLQITSPGOYKEFFPAGGONPEPYLSTFSKEILEA 360
D 342 RIPAGTFYLLNRDNRRNLHIAKFLQITSPGOYKEFFPAGGONPEPYLSTFSKEILEA 401
QY 361 LNTQTERLGVLAGOOREGVIIRASQEOIRELTRDSESRRMHIRGESSRGPNLEFKR 420
D 402 LNTQTERLGVLAGOOREGVIIRASQEOIRELTRDSESRRMHIRGESSRGPNLEFKR 461
QY 421 PLYSNKYGQAYEVPEDYROLQMDVSVFANITOGSMGPFENRSTKVVVVASGADV 480
D 462 PLYSNKYGQAYEVPEDYROLQMDVSVFANITOGSMGPFENRSTKVVVVASGADV 521
QY 481 EMACPHLSGRHGRGGRGRHREEEVHYEVOYRRLSKREALVYLAGHPVYVSSGNL 540
D 522 EMACPHLSGRHGRGGRGRHREEEVHYEVOYRRLSKREALVYLAGHPVYVSSGNL 581
QY 541 LFAFGINQNNHNFFLAGRENNVLOQIEPQAMELAFASKEVEELFNSODESIFPPGPR 600
D 582 LFAFGINQNNHNFFLAGRENNVLOQIEPQAMELAFAPKREVELTNSODESIFPPGPR 641
QY 601 OHQOOSPRSTKQOQPLVSLIDVEGF 625
D 642 OHQOOSPRSTKQOQPLVSLIDVEGF 666

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RESULT 4
Q9SEW4 ID Q9SEW4 PRELIMINARY; PRT; 593 AA.
AC Q9SEW4;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)
DT VICTILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
OS Juglans regia (English walnut).
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eustosids I;
OC Fagales: Juglandaceae; Juglans.
NCBI_TaxId=31240;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SUNLAND; TISSUE=SOMATIC EMBRYO LINE;
RT Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;
RT Identification and cloning of a cDNA encoding a vicillin-like protein,
RT Jug 1 2, from English walnut kernel (Juglans regia): a major food
RT allergen.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF066055; AAF18269.1; -
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -
DR PRAM: PF00546; SeedStore_7s; 1.
FT NON_TER 1 1
SQ SEQUENCE 593 AA: 69990 MW: 9BA127E19A18C0D8 CRC64;

Query Match 39.4%: Score 1310.5; DB 10; Length 593;
Best Local Similarity 44.1%: Pred. No. 4.8e-88;
Matches 273; Conservative 121; Mismatches 166; Indels 59; Gaps 17;

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QY 32 DNGEDPQTEQOQCKRQOESDPRQOQYCORCKEICEE---EEEYNRO----- 78
D 9 ENRPDRPREQYRQCEYCRQOQOQOQOQOQIRCEERLEEDQSRQRERRRRRGVDQDN 68
QY 79 -RDPQOQYEDQCKRQRETEPRHMOICQCKERYKEKQKQKRIEEOOREDEEYEE 137
D 69 PRDEQYEDQCKRQRETEPRHMOICQCKERYKEKQKRIEEOOREDEEYEE----- 112
QY 138 RMKEDGNKRDPOOREYEDCRHNCEOEPRLOYOCORCOBOO-QORHGR-GGDLMPOR 193
D 113 ---GRDRODPQO-QYHRCQRCQOIOESPROMQOQCKEROYKEQOGERGEASPR 167
QY 194 GSGSREYEEGEKOSDNPYFEDERLSTRFTEEGHISYLENFYRSKRLALKNRYLV 253
D 168 ESRGR---EEQOQNNHYTHHSQISRSRHESEBEVYLFERFTEELLGIEYRYVIL 224
QY 254 EAPNAPVLPRLDADAALLVIGRGALKMHRDNRESYNLECGDVI RIPAGTFYLLNR 313
D 225 DANPNTSMPLPHHKDAESVAVVTRGRATLTVSOETRESFNLGCDVIRVAGATVYINQ 284
QY 314 DNNRRLHIAFLQITSPGOYKEFFPAGGONP-EPLYSTSKLEALNTQTERLGV 372
D 285 DSNRLEMYKLDQVNNPQGFREYAAAGARSPQSYLRVESNDILVALNTPRDLRFRF 344
QY 373 QO--QREGVIRIRASQEOIRELTRD--DSESRRMHIRGESSRGPNLEFKRPLYSNKYG 428
D 345 DQOEOQREGVIRIRASQEKRLALSOHMASAGORPW---GRSSSGGPIRLKESPSYQFG 400
QY 429 QAYEVPEDYROLQMDVSVFANITOGSMGPFENRSTKVVVVASGADVEMACPHLS 488
D 401 QFEACPEEHRQLOEMVLNVAEIKRGAMVPHYNSKATVVVVGSTGRYEMACPHVS 460
QY 489 GRHGRGGRGRHREEEV--HYEVOYRRLSKREALVYLAGHPVYVSSGNL 546
D 461 SQ-SYEGQRRQOEEESTRPFQVYARLARLARGDLEVLPADHPATAYASQNNELRLGFDI 519
QY 547 NAQNNHNFFLAGRENNVLOQIEPQAMELAFASKEVEELFNSODESIFPPGPROHQOS 606
D 520 NGENNQDFLAG-QNNINQLEAREAKLSFMRPREIELEFESQMESYFPTER-----QS 574
QY 607 PRSTKQOQPLVSLIDVEGF 625
D 575 RRGQGRDHPPLASIDFAFF 593

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RESULT 5
Q9ZWI3 ID Q9ZWI3 PRELIMINARY; PRT; 810 AA.
AC Q9ZWI3;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DE 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)
OS Cucurbita maxima (Pumpkin) (Winter squash).
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eustosids I;
OC Cucurbitales; Cucurbitaceae; Cucurbita.
NCBI_TaxId=3661;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN=KURUKAWA AMAKURI NANKIN; TISSUE=COVILEDON;
RX MEDLINE=99107919; PubMed=9891029;
RA Yamada K., Shinada T., Kondo M., Nishimura M., Hara-Nishimura I.;
RT Multiple functional proteins are produced by cleaving Asn-Gln bonds
RT of a single precursor by vacuolar processing enzyme.";
RL J. Biol. Chem. 274:2563-2570(1999).
DR EMBL: AB019195; BAA34056.1; -
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -
DR PRAM: PF00546; SeedStore_7s; 1.
DR PRODOM: PD081059; -; 1.
SQ SEQUENCE 810 AA: 97314 MW: A829A3F7542266AB CRC64;

Db 584 EVFRADQDEGFVAGP---EQOSREOEEOE 611

RESULT 9
ID 09M3X6 PRELIMINARY: PRT: 613 AA.

AC 09M3X6: 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CONVICTILIN PRECUSOR.
GN CVC.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I;
OC Fabales; Fabaceae; Papilionoideae; Pisum.
OX NCBI_TaxID=3888;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CV. BIRTE; TISSUE=SEED COTYLEDON;
RA Casey R.;
RT "The sequence of a pea convicilin cDNA."
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ276875; CAB82855.1; -.
KM Signal.
FT CHAIN 1 29 POTENTIAL.
FT CHAIN 30 613 CONVICTILIN.
SQ SEQUENCE 613 AA: 72063 MW; 49AED9F6135DD19 CRC64;

Query Match 25.4%; Score 844.5; DB 10; Length 613;
Best Local Similarity 32.6%; Pred. No. 7.5e-54;
Matches 207; Conservative 122; Mismatches 216; Indels 89; Gaps 15;

Qy 26 IMSKYDNQEDPOTECQOCORCPOQESDPPOQOYQORCKEICEEPEYNNOR----- 79
Db 26 VYVANTDESSRRVPRQORERGOEKEKEKRGEMRPSTEKE--EDEEGQORERGOE 83
Qy 80 -----DPOOYEQOC--RCORRETEPRIMOICQORCERREYERKROOKRYE 125
Db 84 KEERKRGEMRPSTEKEDEEKEKOKYQOREKEDEEKEKOKYQOREKKEKQVQORGEERME 143
Qy 126 EQOREDEEYEREMKRGDKRDPQOREYEDCRHCEQOERPLQYQORCQOERQORHGG 185
Db 144 RE--EDEEGYDDEWRCQSQRREDPEER-----ARLNRHER--TKDRRH--- 183
Qy 186 GDLMDPQSGRYEGEKEKQSDNPYFDEKSLSTRTEEGHISVLENFYGSKLLRAL 245
Db 184 -----QREGEERSESEQERKNRPFLEFSKNFLEFENNGHILRLQRFDRSDLFENL 237
Qy 246 KNYRLVLEANPNFVLPHTLDADAILLVIGRGALKMIRHNRRESYNLECGDVIRIPAG 305
Db 238 QNYRLVLEAKPHTLFLPHIDADILLVLSGKAILTVLSPMDRNSYNLERGDTIKLPAG 297
Qy 306 TFFYLINRNNERLHIAKLOTISTPGQYKEFFPAGQORPEYLLSTFSKEILEALINTQ 365
Db 298 TTSYLVNODDEDLRLVDLVIPVNGKFEAFDLA--KKNQYLRGFSKNILEASYNTRY 355
Qy 366 ERLRGVLGOORE-----GVIIIRASQOJRELTRDSESRMHIRRGESSRPP 413
Db 356 ETEKEVLEEOEKDKRRQOGEETDAIVVSREQIEELKLKSSS---KSLSPSEFP 411
Qy 414 YNLFNKRPLYSNKGQAYEVKPE-DYROLQMDVSVFIANTQSGMMGPFENRSTRKVY 472
Db 412 INLRSHKPEYSNKGFLPEITPEKKYRQLODDLFVSCVEINMGALMLPHYSRAIVLL 471
Qy 473 VASGADVEMACPHLSGRHGGGKRGHEEVEHYE-----QYRARIKREDAIVLAG 526
Db 472 VNEGKNGTELL-----GLKNEQOEREDRERKERNNEVQRYEARLSPDVIIIPAG 519
Qy 527 HPVYVSSGNENULLFAPGINONNHENFLAGERNVLOOIERQAMELAFASRKEVEEL 586
Db 520 HPVAITASSNLML--GGINNENNRNPLSGSDDNVISOIENPVKELTFPGSVQEIINRL 577

Qy 587 ENSQDESIFFPGRHOHQOQSPRSTKQOQPLVSL 620
Db 578 IKMQKSHFANAEPEQKEQO--SQCKRSPSSIL 609

RESULT 10
ID 022120 PRELIMINARY: PRT: 544 AA.
AC 022120: 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE ALPIA SUBUNIT OF BETA CONGLYCININ.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I;
OC Fabales; Fabaceae; Papilionoideae; Glycine.
OX NCBI_TaxID=3847;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CV. WASESUZUNARI;
RA Maryama N., Katsube T., Mada Y., Utsumi S.;
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB008678; BAA23360.1; -.
DR HSSP; P50477; ICAU.
DR MENDEL; 25074; GLYma;1188;25074.
DR INTERPRO; IPR001113; -.
DR PFAM; PF00546; Seedstore_7s; 1.
DR PRODOM; PD081059; -; 1.
SQ SEQUENCE 544 AA: 63296 MW; 048B243929A9C9AB CRC64;

Query Match 24.9%; Score 827; DB 10; Length 544;
Best Local Similarity 32.2%; Pred. No. 1.2e-52;
Matches 187; Conservative 133; Mismatches 192; Indels 68; Gaps 12;

Qy 66 KEICEE---EYNRQDPQOYEQOCQORRETEPRIMOICQORCERREYERKROOK 122
Db 4 KECEGEELPRPRPRQOREPQOGEKEDEDEQPRIPRPRPQOGEHEDEQEE 63
Qy 123 KYEQOREDEEYEREMKRGDKRDPQOREYEDCRHCEQOERPLQYQORCQOERQORH 182
Db 64 WPKKEERKEKSEDEEDEDQERQPRF--RPHQKEERQOEEED--EQQERS 118
Qy 183 GRGGLMDPQSGRYEGEKEKQSDNPYFDEKSLSTRTEEGHISVLENFYGS 237
Db 119 -----ESEDSELRHKNKRPFLGSRFETLKNQYGRIRVLQRFNQ 161
Qy 238 RSKLRLKKNYRLVLEANPNFVLPHTLDADAILLVIGRGALKMIRHNRRESYNLECG 297
Db 162 RSPQLONLDRYILFENSKPNTLLLPNHADADYLLVILNGTALISLVNDDSDRYLQSG 221
Qy 298 DYIRIPAGTFFYLINRNNERLHIAKLOTISTPGQYKEFFPAGQONPEYLLSTFSKEL 357
Db 222 DALRVPSGTTYVVPNDNENLRLLTTLAIPVKKPGRFESFLSTEAQOOSYLGQSSRNL 281
Qy 358 EAALNTQFRELGLV-----GOOR--EGVIIIRASQOJRELTRDSESRMHIRRG 406
Db 282 EASYDTKEEINKVLFPRREGQOGEORLOESYIYEISQOIRALSKRAKSSRRTI--- 338
Qy 407 GESSRQPNVLEFNKRPLYSNKGQAYEVKPEYDYLQMDVSVFIANTQSGMMGPFENR 466
Db 339 -SSEDKPFLRSRDPILYSKLLQKPFETPEKKYRQLODDLFISYDMNGCALLPHFSK 397
Qy 467 STKVYVVASGADVEMACPHLSGRHGGGKRGHEEVEHYEQ-----VARLSKREA 520
Db 398 AIVILVINGDANIELV-----GLKEQOQOEOQOEPQVLEFRKYLRAELSEDI 444
Qy 521 IYVLGHPVYVSSGNENULLFAPGINONNHENFLAGERNVLOOIERQAMELAFASR 580
Db 445 EVIPAGYVVV--NATSNLNFPAIGINENNRNPLSGSDDNVISOIENPVKELTFPGSVQEIINRL 502

QY 581 KEVEELFNQDESIFFPGPPROHQOQSPRSTKQOOPLVSTL 620
DB 503 QAVEELKKNQRESYFVADAPKKEGNKGR--GPLESSIL 540

RESULT 11

Q1674 PRELIMINARY; PRT; 545 AA.
AC Q1674;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE CONVICTILIN PRECURSOR.
OS *Viola nanbonensis*.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; *Viola*.
OX NCBI_TaxID=3912;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COTYLEDON;
RA Koch G., Koenig S., Becker C., Horstmann C., Schlesiher B.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z71986; CA96513.1; -.
DR HSSP: P50477; ICAU.
DR MENDEL: 12432; *Viola*; 1188; 12432.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
DR PRODOM: PD081059; -; 1.
KW Signal; Seed storage protein.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 545 75 GLOBULIN, CONVICTILIN.
SQ SEQUENCE 545 AA; 62810 MW; 459A876F92F5A87E CRC64;

Query Match 24.4%; Score 811; DB 10; Length 545;
Best Local Similarity 34.3%; Pred. No. 1.8e-51;

Matches 196; Conservative 101; Mismatches 204; Indels 70; Gaps 14;

QY 68 ICEEEYENQRPDPOOQYECOCRCQRETEPRHMOICQRCERRYEKRRKQKREE- 126
DB 23 LCYIYANYDGTETPRVYQREGRQGEKEKEKH-----GEMRSHKEAOPGRERW 75
QY 127 QQREDEKYEERKKEGDKRDPOQREYEDCRHCEQOEPRLOYQOCRCOQROHGRG 186
DB 76 ETSEEEERVDYEWGRSQRHEDPEERARE--RYAEERERRRQWE----- 117
QY 187 DLNPNQGGSGRYEEGEEKSD--NPYPDEKSLSTRFTEEGHISYLENFYGRSKLLRA 244
DB 118 -----GEEKGSSKSQERRNPFLFSNKFLLFENENGHIRLQRFDRSLFEN 167
QY 245 LKNYRLVLEENANFVLPHTLDADAILVIGRGALKMHRNDRSYNECGDVIRIPA 304
DB 168 LQNYRLVEYAKRHTTFLPHIDADLLVYLSRALLTVSPDRNSYNLERDITKLPA 227
QY 305 GTTFYLLNRDNNRRLIAKFLQITSTPGQYKEFFPAGQONPEPYLSTFSKEILEALNQ 364
DB 228 GTTSYLLNODDEDRLVYDLSISVNRPKVESFGLSGSKN--QYLNGFISKNILEASLNRK 285
QY 365 TELRGVY-----GQORE-----GVYIRASQOINELTRDDESRMRHIRGCESS 410
DB 286 YEYIEVYLLLEPOOSIGOKRRSQROETNMLVYKSREQVELKRLAKSSS---KKGVSSE 341
QY 411 RGPYNLFNKRPLYSNKGYOAYEYKPE--DYROLQDMQVSFVFINITQGSMMGPFFNRSRK 469
DB 342 FEFPNLRSONPKYSNKGKLFETTPPKKTPOLDLDFVSSVEINSGMLPHYNSRAIV 401
QY 470 VVVASGEADVENACPHLSGRHGGGGRKHEEEVEVHYEYVARARLSKREAIYVLAGHYV 529
DB 402 ILTVNGSGKLE-----LVGKNEQOQREDEQOY--QRYEARLSPGDVYIIPAGHYV 454
QY 530 VFVSSGNEMLLFAFGINAOHNHENTLAGERNVLOOIEPQAMELAFASRKEVEELFNS 589

DB 455 AVASSSMLNLL--GFGINAEHNNQRMFLTGSDDNVISQIENPVKELTFPGSAQGVNRLKN 512
QY 590 QDESIFFPGPPROHQOQSPRSTKQOOPLVSTL 620
DB 513 QEHSHF--ANAEPEQKEGESQRRKRSPISL 541

RESULT 12

Q9SP11 PRELIMINARY; PRT; 489 AA.
AC Q9SP11;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE SUCROSE BINDING PROTEIN HOMOLOG S-64.
GN SBP.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; *Glycine*.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Pedra J.H.F., Delu-Filho N., Pirovani C.P., Contim L.S., Dewey R.E.,
RA Otoni W.C., Fontes E.P.B.;
RT Antisense and sense expression of a sucrose binding protein homologue
RT gene from soybean in transgenic tobacco affects plant growth and
RT carbohydrate partitioning in leaves.;
RL Plant Sci. 0:0-0(1999).
DR EMBL: AF191299; AAF05723.1; -.
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
SQ SEQUENCE 489 AA; 55834 MW; 9BBC0D45DECECD2 CRC64;

Query Match 23.4%; Score 777.5; DB 10; Length 489;
Best Local Similarity 35.0%; Pred. No. 4.5e-49;

Matches 171; Conservative 99; Mismatches 174; Indels 45; Gaps 11;

QY 138 RMKEGDKRDP-----QOREYED-----GRHCEQOEPRLOYQOCRCOQROH 182
DB 27 KIKETEVEDPELVTKKHOQOQOYTESDKRYLCQOCOSMKQERKOVEETREKEERH 86
QY 183 GRGDDLMNPQGGSGRYEEGEEKOSDNPYFDE--RSLSTRFTEEGHISYLENFYGRSKL 241
DB 87 -----QOEHEEODQNPYFTEEDKDFSTRVETEGSIVLKKFTEKSKL 130
QY 242 LRLAKNYRLVLEENANFVLPHTLDADAILVIGRGALKMHRNDRSYNECGDVIR 301
DB 131 LQGENEFLAILAEARHTEVSPRHPFESEVYLFNIKRAVLGLVRESETEKITLEPDMIH 190
QY 302 IPAGTFFYLLNRDNNRRLIAKFLQITSTPGQYKEFFPAGQONPEPYLSTFSKEILEAL 361
DB 191 IPAGTFFYLLNRDNNRRLIAKFLQITSTPGQYKEFFPAGQONPEPYLSTFSKEILEAL 250
QY 362 NQTERLRCVLYGQORGVYIIRASQOINELTRDDESRMRHIRGCESSRGYNLFNKR 421
DB 251 QTPKGLERLFPNQONGSLFKTISRERVALA--PYKSSWMP--GGE--SKAOFNFTSKRP 306
QY 422 LYSNKGQAYEVKPEYDRO--LQDMQVSFVFINITQGSMMGPFFNRSRKVVVVASGEADV 480
DB 307 TFSNGYGRLEVGPDDEKMKLQRLNMLFTNITQSSMSTHYNISATYIALYMDGRGL 366
QY 481 ENACPHLSGRHGGGGRKHEEEVEVHYEYVARARLSKREAIYVLAGHYVSSGNEMLL 540
DB 367 QISCPHMSRSSDSK-----HDKSSPSYHRISADLKPGWVFPVCPHPTVLASKENLL 420
QY 541 LFAFGINAOHNHENTLAGERNVLOOIEPQAMELAFASRKEVEELFNSQDSITFPGR 600
DB 421 IICFEVNVNDNKKFTTFAGKD--NIVSSLDNVAKELAFNPSEYNGVF--ERKESLFPPEL 478
QY 601 QHQOQSPRS 609

Db 479 PSEERGRA 487

RESULT 13

049927 PRELIMINARY; PRT; 483 AA.
AC 049927;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE P54 PROTEIN.
GN P54.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Pisum.
OX NCBI_TaxId=3888;
RN [1]
RP SEQUENCE FROM N.A.
RA Castillo J., Marquez J.A., Franco L., Ballestar E., Rodrigo M.I.;
RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; Y11207; CAAT2090.1; -.
DR HSSP; P50477; ICAU. Pissa; 3005; 28319.
DR MENDEL; 28319; Pissa; 3005; 28319.
DR INTERPRO; IPR000005; -.
DR INTERPRO; IPR001113; -.
DR PFAM; PF00546; Seedstore_7s; 1.
DR PROSITE; PS00041; HTM_ARAC_FAMILY_1; UNKNOWN_1.
DR PRODOM; PD081059; -. 1.
SQ SEQUENCE 483 AA; 54662 MW; 8127BDAA017BF3D CRC64;

Query Match 23.3%; Score 775.5; DB 10; Length 483;
Best local Similarity 30.4%; Pred. No. 6, 2e-49;
Matches 170; Conservative 112; Mismatches 163; Indels 115; Gaps 12;

QY 50 QESDPRQOQYCORCKEICEEEENRORDPOQOYECOCRCORRETERHMOICQORC 109
DB 28 RKEDDE-----LTKCKDC-----DMQOYDEEDK-----ICMERC 60
QY 110 ERYEYKRRKQKRYEEQREDEKYEENKEDNKRDOQREYEDCRHCEQERLQY 169-
DB 61 D-DYIKKQERQNHKEHEEEEOED----- 87
QY 170 OCORRCQEOQRHGRGGLMNPORGSGRYEEGEKQSDNPYYFDERSLSTRTEGHI 229
DB 88 -----ENPYFEEDNDEETKIDTKGRV 109
QY 230 SVLENFYGSKLRALKNRVLLEANPNVLPHTLDADAILVIGRGALMHIRDN 289
DB 110 LILNKNFNEKSKLKNENYGLAVLEIKANAFSPHNYDSFALFNKRGICIGLVAEDRT 169
QY 290 ESNALGCVIRIPAGTTFYLLINRDNRRHLIAKF---LQITSPQOYKEFFPAGQNE 346
DB 170 ERNLLEGGDMRPVAPATPVYLRDENEXLYIAAFMPPSSGSAVNLPEFFESAGRKPE 229
QY 347 PYLSTESKEILEALNTQTERLGVLAGOOREGYIIRASOEQIRELTRDSESRMHIRG 406
DB 230 SVLNTSSKVLQALAKSSNGELETVDQKGRIFIEKEDVGLAPKSS---LWPF--- 283
QY 407 GESSRQPYLNFNRPYLSNKGAYEVKPEDYRQ-LQDMQSVFANITQSGMGEFENT 465
DB 284 GGFKSPFNIIFSNNPAFSNKFGLFEVGPSEKSGLEGINTLMLTLANITKGSMTIHYN 343
QY 466 RSTKVVYVSGEADVMACPHSGRIGRGCGKRHEEEVHYEYRARRLSKEALIVLA 525
DB 344 NAKKTALVTDGEBELMACPHPS-----SSNSRQKSSISITHINAKLRPGVMFVPR 398
QY 526 GHPVYVSSGENTLLFAGINAOHNHNFLAGRERNVLOQLEPQAMELAFASRKEVER 585
DB 399 GHPFVIAKKKKKLLIVVCEVYVNAQRNKKLALAK-KNYSALDKAKKVAFDIAAKVDE 457

QY 586 LFNSODESIFPPGPROHQO 605
DB 458 VFERKEE-FFPPYDNERKE 476

RESULT 14

022121 PRELIMINARY; PRT; 417 AA.
AC 022121;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE BETA SUBUNIT OF BETA CONGLYCININ.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Glycine.
OX NCBI_TaxId=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-CV, WASESUUNARI;
RA Maruyama N., Katsube T., Mada Y., De la Rosa A., Utsuni S.;
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB008679; BAA23361.1; -.
DR HSSP; P02853; 2PHL.
DR MENDEL; 25075; Glyma; 1188; 25075.
DR INTERPRO; IPR001113; -.
DR PFAM; PF00546; Seedstore_7s; 1.
DR PRODOM; PD081059; -. 1.
SQ SEQUENCE 417 AA; 48106 MW; DDEE50B5B779556E CRC64;

Query Match 22.8%; Score 758; DB 10; Length 417;
Best local Similarity 38.0%; Pred. No. 9, 7e-48;
Matches 163; Conservative 87; Mismatches 145; Indels 34; Gaps 7;

QY 205 KQSDNPYF-DEKSLSTRTEEGHISVLENFYGSKLRALKNRVLLEANPNVLP 263
DB 6 EDENPFYFRSSSFQTLFENQNGRIRLLQRFNKRSPQLENLRDVRIVOFOSKPNITLLP 65
QY 264 THLDADAILLVIGRGALMHIRDNRESYNLBCGVIRIPAGTTFYLLINRDNRRHLIAK 323
DB 66 HHADAPFLFLVLSGRAILTLVNNDDRSYNLHPGDQRIIPAGTTFYLLVPHDHQNLTKIK 125
QY 324 FLQITSPQOYKEFFPAGQNEPYPYLSFESKEILEALNTQTERLGVL-----GQOR 377
DB 126 LAIPVKKPGRYDPLFSSNQAOQSYLQGFSHNILETSFSEEEINRVLFGEEDGRQOE 185
QY 378 GYIIRASQEIRELTRDSESRMHIRGESSRQPYLNFNRPYLSNKGAYEVKPED 437
DB 186 GYIVELSKQIROLISRRAKSSSKRTI---SSDEDFNRSRNPYISNMFGRFFETTPER 241
QY 438 YRQLODMQSVFANITQSGMGPFPNTSTKVVVAVSGEADVMACPHLSGHRGCG 497
DB 242 NPQLRDLDFLSSVDINBALLPFNFSKAIYILVINEGDANIELV-----G 288
QY 498 -----KRHEEEVHYEYRARRLSKEALIVLAGHPVYVSSGENTLLFAGINAOHN 551
DB 289 IKRQOQKQOEPEPLVQGYRAELSEDVFIIPAAYF--FVNATSNLNPFLAFGIAENN 346
QY 552 HENFLAGRERNVLOQLEPQAMELAFASRKEVEBELFNSODESIFPPGPROHQOQSRSTK 611
DB 347 ORNFLAGEKDNVVRQIROVOELAFPGSAQDVERLLKKORESYFYDA--QPOOKEGSGK 404
QY 612 OQOPLVSTIL 620
DB 405 RKQPPSIL 413

RESULT 15
043626 PRELIMINARY; PRT; 438 AA.
ID 043626
AC 043626;

